

# SEQUENCE LISTING

<110> Duke University  
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<120> GENERATION OF RECOMBINANT ADENO-ASSOCIATED VIRAL VECTORS BY A  
COMPLETE ADENOVIRUS-MEDIATED APPROACH

<130> 180/137

<150> US 60/349,532

<151> 2002-01-18

<160> 22

<170> PatentIn version 3.2

<210> 1

<211> 1611

<212> DNA

<213> adeno-associated virus 2

<220>

<221> CDS

<222> (1)..(1611)

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gag cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag	96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	
20 25 30	
aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att	144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	
35 40 45	
gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg	192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	
50 55 60	
acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg	240
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	
65 70 75 80	
caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa	288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
85 90 95	
acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att	336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
100 105 110	
cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg	384
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
115 120 125	
cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg	432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	
130 135 140	
aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aaa	480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys	
145 150 155 160	

acc cag cct gag ctc cag tgg gcg tgg act aat atg gaa cag tat tta	528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu	
165 170 175	
agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat	576
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His	
180 185 190	
ctg acg cac gtg tgc cag acg gag gag cag aac aaa gag aat cag aat	624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn	
195 200 205	
ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac	672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr	
210 215 220	
atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag	720
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
225 230 235 240	
cag tgg atc cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc	768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
245 250 255	
tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag	816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
260 265 270	
att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag	864
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
275 280 285	
ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta	912
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
290 295 300	
aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc	960
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
305 310 315 320	
acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca	1008
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	
325 330 335	
act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc	1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro	
340 345 350	
ttc tac ggg tgc gta aac tgg acc aat gag aac ttt ccc ttc aac gac	1104
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp	
355 360 365	
tgt gtc gac aag atg gtg atc tgg tgg gag gag ggg aag atg acc gcc	1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala	
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg	
385 390 395 400	
gtg gac cag aaa tgc aag tcc tgc gcc cag ata gac ccg act ccc gtg	1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val	
405 410 415	
atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac tca	1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	
420 425 430	

acg acc ttc gaa cac cag cag ccg ttg caa gac cgg atg ttc aaa ttt	1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	
435 440 445	
gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag	1392
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	
450 455 460	
gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg	1440
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val	
465 470 475 480	
gag cat gaa ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc	1488
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala	
485 490 495	
ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt	1536
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val	
500 505 510	
gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gac	1584
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp	
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aga ttg gct cga gga cac tct ctc tga	1611
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 <212> PRT  
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<400> 2

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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	
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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	
50 55 60	
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	
65 70 75 80	
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
85 90 95	
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
100 105 110	
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
115 120 125	

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
450 455 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
465 470 475 480

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
485 490 495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
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<222> (1)..(1866)

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Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
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aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att 144  
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
35 40 45  
gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg 192  
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
50 55 60  
acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg 240  
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
65 70 75 80

caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa	288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
85 90 95	
acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att	336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
100 105 110	
cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg	384
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
115 120 125	
cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg	432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	
130 135 140	
aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aag	480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys	
145 150 155 160	
acc cag cct gaa ctg cag tgg gcg tgg act aat atg gaa cag tat tta	528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu	
165 170 175	
agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat	576
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His	
180 185 190	
ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat	624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn	
195 200 205	
ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac	672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr	
210 215 220	
atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag	720
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
225 230 235 240	
cag tgg ata cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc	768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
245 250 255	
tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag	816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
260 265 270	
att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag	864
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
275 280 285	
ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta	912
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
290 295 300	
aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc	960
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
305 310 315 320	
acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca	1008
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	
325 330 335	
act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc	1056
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340 345 350	

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gtg gac cag aaa tgc aag tcc tcg gcc cag ata gac ccg act ccc gtg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415	1248
atc gtc acc tcc aac acc aat atg tgc gcc gtg att gac ggg aac tca Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430	1296
acg acc ttc gaa cac cag cag ccg ttg caa gac cgg atg ttc aaa ttt Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445	1344
gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460	1392
gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480	1440
gag cat gag ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495	1488
ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510	1536
gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gat Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525	1584
aga tac caa aac aaa tgt tct cgt cac gtg ggc atg aat ctg atg ctg Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540	1632
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ttc act cac gga cag aaa gac tgt tta gag tgc ttt ccc gtg tca gaa Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575	1728
tct caa ccc gtt tct gtc gtc aaa aag gcg tat cag aaa ctg tgc tac Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590	1776
att cat cat atc atg gga aag gtg cca gac gct tgc act gcc tgc gat Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605	1824
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 <213> adeno-associated virus 2

<400> 4

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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240



Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
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 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
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 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
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 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
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 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
515 520 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
530 535 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
545 550 555 560

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
565 570 575

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
580 585 590

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
595 600 605

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<213> adeno-associated virus 2

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gctggtcggg tggctcgtgg acaaggggat tacctcggag aagcagtgga tccaggagga 180  
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ctgcagacaa	tgcgagagaa	tgaatcagaa	ttcaaatac	tgcttcactc	acggacagaa	1140
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ctccgggaaa	aaagaggccg	gtagagcact	ctcctgtgga	gccagactcc	tctcgggaa	1800
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cagactcagt	acctgacccc	cagcctctcg	gacagccacc	agcagccccc	tctggtctgg	1920
gaactaatac	gatggctaca	ggcagtggcg	caccaatggc	agacaataac	gagggcgccg	1980
acggagtggg	taattcctcg	ggaaattggc	attgcgattc	cacatggatg	ggcgacagag	2040
tcatcaccac	cagcaccgga	acctgggccc	tgcccaccta	caacaaccac	ctctacaaac	2100
aaatttccag	ccaatcagga	gcctcgaacg	acaatcacta	ctttggctac	agcaccctt	2160
gggggtattt	tgacttcaac	agattccact	gccacttttc	accacgtgac	tggcaaagac	2220
tcatcaacaa	caactgggga	ttccgaccca	agagactcaa	cttcaagctc	tttaacattc	2280
aagtcaaaga	ggtcacgcag	aatgacggta	cgacgacgat	tgccaataac	cttaccagca	2340
cggttcaggt	gtttactgac	tcggagtacc	agctcccgtg	cgctctcggc	tcggcgcatc	2400
aaggatgcct	cccgcggttc	ccagcagacg	tcttcatggg	gccacagtat	ggatacctca	2460
ccctgaacaa	cgggagtcag	gcagtaggac	gctcttcatt	ttactgcctg	gagtactttc	2520
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accagtacct	gtattacttg	agcagaacaa	acactccaag	tggaaccacc	acgcagtcaa	2700
ggcttcagtt	ttctcaggcc	ggagcgagtg	acattcgggg	ccagtctagg	aactggcttc	2760
ctggaccctg	ttaccgccag	cagcgagtat	caaagacatc	tgcggtatac	aacaacagtg	2820
aatactcgtg	gactggagct	accaagtacc	acctcaatgg	cagagactct	ctggtgaatc	2880
cgggcccggc	catggcaagc	cacaaggacg	atgaagaaaa	gttttttctc	cagagcgggg	2940
ttctcatctt	tgggaagcaa	ggctcagaga	aaacaaatgt	ggacattgaa	aaggtcatga	3000
ttacagacga	agaggaaatc	aggacaacca	atcccgtggc	tacggagcag	tatggttctg	3060

tatctaccaa cctccagaga ggcaacagac aagcagctac cgcagatgtc aacacacaag 3120  
 gcggttcttcc aggcattggtc tggcaggaca gagatgtgta ccttcagggg cccattctggg 3180  
 caaagattcc acacacggac ggacattttc acccctctcc cctcatgggt ggattcggac 3240  
 ttaaacaccc tctccacag attctcatca agaacacccc ggtacctgcy aatccttcga 3300  
 ccaccttcag tgcggcaaag ttgcttcct tcatcacaca gtactccacg ggacagggtca 3360  
 gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa acgctggaat cccgaaattc 3420  
 agtacacttc caactacaac aagtctgtta atgtggactt tactgtggac actaatggcg 3480  
 tgtattcaga gcctcgcccc attggcacca gatacctgac tcgtaatctg taattgcttg 3540  
 ttaatcaata aaccgttta ttcgtttcag ttga 3574

<210> 6  
 <211> 312  
 <212> PRT  
 <213> adeno-associated virus 2

<400> 6

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
290 295 300

Arg Leu Ala Arg Gly His Ser Leu  
305 310

<210> 7  
<211> 397  
<212> PRT  
<213> adeno-associated virus 2

<400> 7

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
50 55 60

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 8  
 <211> 2478  
 <212> DNA  
 <213> adeno-associated virus 2

<400> 8  
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 aaaacaaatg ttctcgtcac gtgggcatga atctgatgct gtttcctgc agacaatgcg 120  
 agagaatgaa tcagaattca aatatctgct tcactcacgg acagaaagac tgttttagagt 180  
 gctttcccgt gtcagaatct caaccggtt ctgtcgtaa aaaggcgat cagaaactgt 240  
 gctacattca tcatatcatg ggaaagggtgc cagacgcttg cactgcctgc gatctggtca 300  
 atgtggattt ggatgactgc atctttgaac aataaatgat ttaaatacagg tatggctgcc 360  
 gatggttatc ttccagattg gctcgaggac actctctctg aaggaataag acagtgggtgg 420  
 aagctcaaac ctggcccacc accaccaaag cccgcagagc ggcataagga cgacagcagg 480  
 ggtcttggtgc ttctgggta caagtacctc ggacccttca acggactcga caagggagag 540  
 ccggtcaacg aggcagacgc cgcggccctc gagcacgaca aagcctacga ccggcagctc 600  
 gacagcggag acaaccgta cctcaagtac aaccacgccg acgcggagtt tcaggagcgc 660  
 cttaaagaag atacgtcttt tgggggcaac ctcgagcagc cagtcttcca ggcgaaaaag 720  
 agggttcttg aacctctggg cctgggtgag gaacctgtta agacggctcc gggaaaaaag 780  
 aggccggtag agcactctcc tgtggagcca gactcctcct cgggaaccgg aaaggcgggc 840  
 cagcagcctg caagaaaaag attgaatttt ggtcagactg gagacgcaga ctacgtacct 900  
 gacccccagc ctctcggaca gccaccagca gccccctctg gtctgggaac taatacgtatg 960  
 gctacaggca gtggcgacac aatggcagac aataacgagg gcgccgacgg agtgggtaat 1020  
 tcctcgggaa attggcattg cgattccaca tggatgggag acagagtcac caccaccagc 1080  
 acccgaacct gggccctgcc cacctacaac aaccacctct acaacaaat ttccagccaa 1140  
 tcaggagcct cgaacgacaa tcaactctt ggctacagca ccccttgggg gtattttgac 1200  
 ttcaacagat tccactgcca cttttacca cgtgactggc aaagactcat caacaacaac 1260  
 tggggattcc gacccaagag actcaacttc aagctcttta acattcaagt caaagaggtc 1320  
 acgcagaatg acggtacgac gacgattgcc aataacctta ccagcacggc tcagggtgttt 1380  
 actgactcgg agtaccagct cccgtacgtc ctcggtcggc cgcatacagg atgcctcccg 1440  
 ccgttcccag cagacgtctt catggtgccca cagtatggat acctaccct gaacaacggg 1500  
 agtcaggcag taggacgctc ttcattttac tgcttgaggt actttccttc tcagatgctg 1560  
 cgtaccgga acaactttac cttcagctac acttttgagg acgttccttt ccacagcagc 1620

tacgctcaca gccagagtct ggaccgtctc atgaatcctc tcatcgacca gtacctgtat 1680  
 tacttgagca gaacaaacac tccaagtgga accaccacgc agtcaaggct tcagttttct 1740  
 caggccggag cgagtgacat tcgggaccag tctaggaact ggcttcctgg accctgttac 1800  
 cgccagcagc gagtatcaaa gacatctgcg gataacaaca acagtgaata ctcgtggact 1860  
 ggagctacca agtaccacct caatggcaga gactctctgg tgaatccggg cccggccatg 1920  
 gcaagccaca aggacgatga agaaaagttt tttcctcaga gcgggggttct catctttggg 1980  
 aagcaaggct cagagaaaac aaatgtggac attgaaaagg tcatgattac agacgaagag 2040  
 gaaatcagga caaccaatcc cgtggctacg gagcagtatg gttctgtatc taccaacctc 2100  
 cagagaggca acagacaagc agctaccgca gatgtcaaca cacaaggcgt tcttccaggc 2160  
 atggtctggc aggacagaga tgtgtacctt cagggggccca tctgggcaaa gattccacac 2220  
 acggacggac attttcaccc ctctcccctc atgggtggat tcggacttaa acaccctcct 2280  
 ccacagattc tcatcaagaa caccocggta cctgcgaatc cttcgaccac cttcagtgcg 2340  
 gcaaagtttg cttccttcat cacacagtac tccacgggac aggtcagcgt ggagatcgag 2400  
 tgggagctgc agaaggaaaa cagcaaacgc tggaatcccg aaattcagta cacttccaac 2460  
 tacaacaagt ctgttaat 2478

<210> 9  
 <211> 735  
 <212> PRT  
 <213> adeno-associated virus 2

<400> 9

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125



Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 10  
<211> 598  
<212> PRT  
<213> adeno-associated virus 2  
<400> 10

Met Ala Pro Gly Lys Lys Arg Pro Val Glu His Ser Pro Val Glu Pro  
1 5 10 15

Asp Ser Ser Ser Gly Thr Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys  
20 25 30

Arg Leu Asn Phe Gly Gln Thr Gly Asp Ala Asp Ser Val Pro Asp Pro  
35 40 45

Gln Pro Leu Gly Gln Pro Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn  
50 55 60

Thr Met Ala Thr Gly Ser Gly Ala Pro Met Ala Asp Asn Asn Glu Gly  
65 70 75 80

Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr  
85 90 95

Trp Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
100 105 110

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly  
115 120 125

Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
130 135 140

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln  
145 150 155 160

Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe  
165 170 175

Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Asp Gly Thr  
 180 185 190  
 Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp  
 195 200 205  
 Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys  
 210 215 220  
 Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr  
 225 230 235 240  
 Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr  
 245 250 255  
 Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe  
 260 265 270  
 Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala  
 275 280 285  
 His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr  
 290 295 300  
 Leu Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln  
 305 310 315 320  
 Ser Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln  
 325 330 335  
 Ser Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser  
 340 345 350  
 Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala  
 355 360 365  
 Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro  
 370 375 380  
 Ala Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser  
 385 390 395 400  
 Gly Val Leu Ile Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp  
 405 410 415  
 Ile Glu Lys Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn  
 420 425 430  
 Pro Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg  
 435 440 445

Gly Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu  
 450 455 460

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
 465 470 475 480

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu  
 485 490 495

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
 500 505 510

Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys  
 515 520 525

Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
 530 535 540

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
 545 550 555 560

Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr  
 565 570 575

Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
 580 585 590

Tyr Leu Thr Arg Asn Leu  
 595

<210> 11  
 <211> 533  
 <212> PRT  
 <213> adeno-associated virus 2  
 <400> 11

Met Ala Thr Gly Ser Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala  
 1 5 10 15

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp  
 20 25 30

Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
 35 40 45

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala  
 50 55 60

Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe  
 65 70 75 80

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Glu Lys Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro  
 355 360 365  
 Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly  
 370 375 380  
 Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro  
 385 390 395 400  
 Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp  
 405 410 415  
 Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met  
 420 425 430  
 Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn  
 435 440 445  
 Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe  
 450 455 460  
 Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile  
 465 470 475 480  
 Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile  
 485 490 495  
 Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val  
 500 505 510  
 Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr  
 515 520 525  
 Leu Thr Arg Asn Leu  
 530

<210> 12  
 <211> 145  
 <212> DNA  
 <213> adeno-associated virus 2  
  
 <400> 12  
 ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60  
 cgacgcccg gctttgccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg 120  
 gccaaactcca tcaactagggg ttctt 145  
  
 <210> 13  
 <211> 144  
 <212> DNA  
 <213> adeno-associated virus 2  
  
 <400> 13  
 ggaacccta gtgatggagt tggccactcc ctctctgcgc gctcgctcgc tcaactgaggc 60

cgggcgacca aaggtcgccc gacgcccggg ctttgcccgg gcggcctcag tgagcgagcg 120  
agcgcgcaga gagggagtgg ccaa 144

<210> 14  
<211> 31  
<212> DNA  
<213> adeno-associated virus

<220>  
<221> misc\_feature  
<222> (1)..(31)  
<223> corresponds to base pairs 318-339 of AAV with an EcoR V site at the 5' end

<400> 14  
gatatcgcca tgccgggggtt ttacgagatt g 31

<210> 15  
<211> 35  
<212> DNA  
<213> adeno-associated virus

<220>  
<221> misc\_feature  
<222> (1)..(35)  
<223> corresponds to base pairs 1812 to 1846 of AAV

<220>  
<221> mutation  
<222> (20)..(20)

<220>  
<221> mutation  
<222> (23)..(23)

<400> 15  
gcaccggttt gggctcactg atgtctgcgt cactg 35

<210> 16  
<211> 35  
<212> DNA  
<213> adeno-associated virus

<220>  
<221> misc\_feature  
<222> (1)..(35)  
<223> corresponds to base pairs 1812 to 1846 of AAV

<220>  
<221> mutation  
<222> (13)..(13)

<220>  
<221> mutation  
<222> (16)..(16)

<400> 16  
cagtgcgcga gacatcagtg agcccaaacg ggtgc 35



<210> 17  
 <211> 29  
 <212> DNA  
 <213> adeno-associated virus

<220>  
 <221> misc\_feature  
 <222> (1)..(29)  
 <223> corresponds to base pairs 2261 to 2289 of AAV

<400> 17  
 tgggccaggt ttgagcttcc accactgtc 29

<210> 18  
 <211> 55  
 <212> DNA  
 <213> adeno-associated virus

<220>  
 <221> misc\_feature  
 <222> (1)..(27)  
 <223> corresponds to base pairs 2261-2289 of AAV

<220>  
 <221> misc\_feature  
 <222> (28)..(53)  
 <223> corresponds to base pairs 4330-4355 of AAV

<400> 18  
 gacagtgggtg gaagctcaaa cctggcccaa gcacctgaat ggcacctatg attac 55

<210> 19  
 <211> 28  
 <212> DNA  
 <213> adeno-associated virus

<220>  
 <221> misc\_feature  
 <222> (1)..(28)  
 <223> corresponds to base pairs 4446-4467 of AAV with a BamHI site at the 3' end

<400> 19  
 ggatcccgca gagaccaaag ttcaactg 28

<210> 20  
 <211> 27  
 <212> DNA  
 <213> adeno-associated virus

<220>  
 <221> misc\_feature  
 <222> (1)..(27)  
 <223> corresponds to base pairs 1852 to 1878, BamHI site at the 5' end

<400> 20  
 agtcagttgc gcagccatcg acgtcag 27

<210> 21  
 <211> 35

<212> DNA  
 <213> adeno-associated virus

<220>  
 <221> misc\_feature  
 <222> (1)..(35)  
 <223> corresponds to base pairs 4302 to 4329, with a Not I site at the  
 3' end

<400> 21  
 gcggccgctt aacagacttg ttgtagttgg aagtg 35

<210> 22  
 <211> 592  
 <212> DNA  
 <213> Homo sapiens

<400> 22  
 gcgtgaagag ctgcagtgct actcttaaag ctgaattaat ctctgccatt ccttaaggaa 60  
 acaggcaact gtcttaaaac cgtgggtttg aaaatatattt gttcaagata aaactgtttt 120  
 aagatatatg tatatatatc ttatatatct gtattcgcat ggtaacatat cttcgggtctt 180  
 cctgccgctg ggctctcagc ggccctccaa ggcagcccgc aggcccgctg tgcctcagg 240  
 gatcctccac agccccgggg agaccttgcc tctaaagttg ctgcttttgc agctctgcca 300  
 caaccgcgcg tcctcagagc cagccgggag gagctagaac cttccccgcg tttctttcag 360  
 cagccctgag tcagaggcgg gctggccttg caagtagccg ccagccttc ttcggtctca 420  
 cggaccgatc cgcccgaacc ttctcccggg gtcagcgccg cgctgcgccg cccggctgac 480  
 tcagcccggg cgggcgggcg ggaggctctc gactgggcgg gaaggcgcg gaaggttcgc 540  
 ggcggcgggg tcggggaggt gcaaaaggat gaaaagcccg tggacggagc tg 592